

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,429

DATE: 12/14/2001

TIME: 11:11:19

Input Set : A:\241421.txt

Output Set: N:\CRF3\12142001\I005429.raw

ENTERED

3 <110> APPLICANT: Sewalt, Vincent
 4 Hastings, Craig
 5 Meeley, Robert
 6 Hantke, Sabine
 7 Jung, Rudolf
 8 Everard, John
 9 Allen, Stephen

11 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS
 OF PROTEINS

13 <130> FILE REFERENCE: 5718-119 (035718/241421)
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/005,429
 C--> 15 <141> CURRENT FILING DATE: 2001-12-03
 15 <150> PRIOR APPLICATION NUMBER: 60/250,703
 16 <151> PRIOR FILING DATE: 2000-12-01
 18 <160> NUMBER OF SEQ ID NOS: 25
 20 <170> SOFTWARE: PatentIn version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 797
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Zea mays
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (187)..(573)
 31 <400> SEQUENCE: 1

32	gcacgagcat gtgtttccta gaaataatca atatattgag ataaatctca atcaatatat	60
34	tgattatttc taggaacac atgccggaat gagggcacca ttatccgcgt ccagtggtgc	120
36	cgctactccg ctcccctca gtcctcagtt cctcacctag cggtagcgtg cgcgcgggag	180
38	acgtag atg gcg gct tcg gag gcg gca gcg gcg gcg gca aca ccg gtg	228
39	Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val	
40	1 5 10	
42	acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg	276
43	Thr Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp	
44	15 20 25 30	
46	agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att	324
47	Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile	
48	35 40 45	
50	gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att	372
51	Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile	
52	50 55 60	
54	ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt	420
55	Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val	
56	65 70 75	
58	gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc	468
59	Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala	
60	80 85 90	
62	atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc	516
63	Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val	
64	95 100 105 110	

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66 gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg      564
67 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
68              115              120              125
70 gcc tcg tag atcagtgatg ccgtaatgta gtattcgccct aaataagagg      613
71 Ala Ser
74 acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag      673
76 tgcccccttt ggtggtactt cttcgatatgt agtattaact cctgtcttaa tatgttgccc      733
78 tgcttgtgct ttccatacca tgtttgctct ttcagctgag gtgttaaaaa aaaaaaaaaa      793
80 aaaa      797
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 128
85 <212> TYPE: PRT
86 <213> ORGANISM: Zea mays
88 <400> SEQUENCE: 2
90 Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Thr Pro Val Thr Pro
91 1              5              10              15
94 Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
95              20              25              30
98 Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
99              35              40              45
102 Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
103              50              55              60
106 Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
107 65              70              75              80
110 Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
111              85              90              95
114 Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
115              100              105              110
118 Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
119              115              120              125
122 <210> SEQ ID NO: 3
123 <211> LENGTH: 799
124 <212> TYPE: DNA
125 <213> ORGANISM: Zea mays
127 <220> FEATURE:
128 <221> NAME/KEY: CDS
129 <222> LOCATION: (69)..(455)
131 <400> SEQUENCE: 3
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134 agacgtag atg gcg gct tcg gag gcg gcg gcg gcg gcg gca ccg gtg      110
135      Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Thr Pro Val
136      1              5              10
138 gcg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg      158
139 Ala Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp
140 15              20              25              30
142 agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att      206
143 Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile
144              35              40              45
146 gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att      254

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147 Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile
148          50          55          60
150 ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt      302
151 Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val
152          65          70          75
154 gat gtc gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc      350
155 Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala
156          80          85          90
158 atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc      398
159 Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val
160 95          100          105          110
162 gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg      446
163 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met
164          115          120          125
166 gcc tcg tag atcagtgatg ccgtaatgta gtattcgctt aaataagagg      495
167 Ala Ser
170 acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag      555
172 tgcccccttt ggtggtactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc      615
174 tgcttgctgt tttcatacca tgtttgctct ttcagctgag gtgttatatcg gtaaatcgga      675
176 gtcaatatct ttgaaattga ttaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      735
178 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      795
180 aaaa      799
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 128
185 <212> TYPE: PRT
186 <213> ORGANISM: Zea mays
188 <400> SEQUENCE: 4
190 Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Thr Pro Val Ala Pro
191 1          5          10          15
194 Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile
195          20          25          30
198 Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe
199          35          40          45
202 Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala
203          50          55          60
206 Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val
207 65          70          75          80
210 Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro
211          85          90          95
214 Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly
215          100          105          110
218 Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser
219          115          120          125
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 367
224 <212> TYPE: DNA
225 <213> ORGANISM: Zea mays
227 <220> FEATURE:
228 <221> NAME/KEY: CDS

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229 <222> LOCATION: (3)..(194)
231 <400> SEQUENCE: 5
232 cc cgc ttc tcc gac gcc atc ttc gtc aag gtc gac gtc gac gag ctc      47
233   Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu
234   1           5           10           15
236 gcg gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gta      95
237 Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val
238           20           25           30
240 ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag      143
241 Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys
242           35           40           45
244 gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg      191
245 Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
246           50           55           60
248 taa actcctgtgg ttgcctggg acggagtgc tgaagtgaatg tggtccttc      244
250 tctcaatgct gaaaaaaggg ggaaaaacta tgtgaaatg atggtagacg tgtctgggctc      304
252 agtaataaga gtttctaaaa tctgaatgag atttgaatcg ctttcogttg ctgaaaaaaa      364
254 aaa      367
257 <210> SEQ ID NO: 6
258 <211> LENGTH: 63
259 <212> TYPE: PRT
260 <213> ORGANISM: Zea mays
262 <400> SEQUENCE: 6
264 Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala
265 1           5           10           15
268 Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
269           20           25           30
272 Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp
273           35           40           45
276 Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser Ser
277           50           55           60
280 <210> SEQ ID NO: 7
281 <211> LENGTH: 720
282 <212> TYPE: DNA
283 <213> ORGANISM: Zea mays
285 <220> FEATURE:
286 <221> NAME/KEY: CDS
287 <222> LOCATION: (38)..(442)
289 <400> SEQUENCE: 7
290 aggcagcgag tgcaaacaac cgcgagagcg atcagcg atg ggc tcc ttc ttc tcg      55
291           Met Gly Ser Phe Phe Ser
292           1           5
294 acc tta gtg acg ccc cct ccg ccc gcc gcc gac gac ccg aac tgc gcc      103
295 Thr Leu Val Thr Pro Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala
296           10           15           20
298 gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc      151
299 Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala
300           25           30           35
302 cac aag agc agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg      199

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303 His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp
304      40                      45                      50
306 tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc      247
307 Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser
308 55                      60                      65                      70
310 cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctg gcg      295
311 Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala
312                      75                      80                      85
314 gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg      343
315 Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu
316      90                      95                      100
318 gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac      391
319 Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp
320      105                      110                      115
322 gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc      439
323 Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser Ser
324      120                      125                      130
326 taa cttagcagtg catacactcc caccttatta ctggtttctc gactccagtg      492
328 gttcgcctgg gacgggggttg ctgaaatggt tcccttctct gaatactgaa aaatcaaaaa      552
330 aagaagtata tgaaaaaatg atggtagacg tgtctgggtc aataagagtt tctgaaactt      612
332 ggatttgat gtgtcagtt ctgtgttctg ttccaagga atggatcatg tgagtttgga      672
334 atatagctgg aaatatgttg tgctgttaaa aaaaaaaaaa aaaaaaaaaa      720
337 <210> SEQ ID NO: 8
338 <211> LENGTH: 134
339 <212> TYPE: PRT
340 <213> ORGANISM: Zea mays
342 <400> SEQUENCE: 8
344 Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala
345 1                      5                      10                      15
348 Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr
349      20                      25                      30
352 Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile
353      35                      40                      45
356 Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala
357      50                      55                      60
360 Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val
361 65                      70                      75                      80
364 Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala
365      85                      90                      95
368 Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val
369      100                      105                      110
372 Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val
373      115                      120                      125
376 Thr Ser Ser Ser Ser Ser
377      130
380 <210> SEQ ID NO: 9
381 <211> LENGTH: 722
382 <212> TYPE: DNA
383 <213> ORGANISM: Zea mays

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:775 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:777 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:783 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:787 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:789 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:791 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18